

# SEQUENCE LISTING

<110> Kaia Palm  
Tonis Timmusk  
CeMines Research

<120> MAMMALIAN NEURALIZED FAMILY OF  
TRANSCRIPTION REGULATORS AND USES THEREFOR

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<212> DNA

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<210> 10  
 <211> 557  
 <212> PRT  
 <213> mouse

<400> 10  
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 1 5 10 15  
 Ser Phe Pro Val Pro Ser His Arg Cys His His Lys Gln Lys His Cys  
 20 25 30  
 Pro Pro Thr Leu Ser Gly Gly Gly Leu Pro Ala Thr Pro Leu Leu Phe



Ala Pro Asn Ser Pro Val Ser Leu Pro Glu Ser Pro Val Thr Pro Gly  
485 490 495  
Leu Gly Gln Trp Ser Asp Glu Cys Thr Ile Cys Tyr Glu His Ala Val  
500 505 510  
Asp Thr Val Ile Tyr Thr Cys Gly His Met Cys Leu Cys Tyr Ser Cys  
515 520 525  
Gly Leu Arg Leu Lys Lys Ala Leu His Ala Cys Cys Pro Ile Cys Arg  
530 535 540  
Arg Pro Ile Lys Asp Ile Ile Lys Thr Tyr Arg Ser Ser  
545 550 555

<210> 11  
<211> 1035  
<212> DNA  
<213> mouse

<400> 11  
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cgatgccatc acaagcagaa gcattgcccg cctacgctgt caggtggggg gctcccggcc 180  
acgccgctgc tcttccaccc ccacactaag ggctcccaga tcctcatgga cctcagccac 240  
aaggccgtca agaggcaggc cagcttctgc aatgccatca ccttcagtaa ccgcccgggtg 300  
ctcatctacg agcaagtcag gctgaagatc accaagaagc aatgctgctg gagcggggcc 360  
ctgcgacttg gcttcaccag caaggaccct tcccgcatcc accccgactc gctgcccag 420  
tacgctgcc ctgacctggg gtctcagagt ggcttctggg ccaaagcatt gcctgaggag 480  
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cggatcaatg agtcagctgc tatgcttttc ttcagtgggg tccggacggg ggacccgctc 600  
tgggccctgg tggacgtcta cggcctcacg cgggggtgtc agctgctagg ctccaccatc 660  
atgactgaac ggggtggccc atctctcccc tgcacactg cttccactcc aacctacccc 720  
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accccggtc tggggcagtg gagtgatgaa tgcaccattt gctatgaaca cgcagtggat 900  
acagtcatct acacgtgtgg ccacatgtgc ctgtgtact cctgtggcct gcgcctcaag 960  
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taccgcagct cgtag 1035

<210> 12  
<211> 344  
<212> PRT  
<213> mouse

<400> 12  
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Gly Ser Phe Pro Val Pro Ser His Arg Cys His His Lys Gln Lys His  
35 40 45  
Cys Pro Pro Thr Leu Ser Gly Gly Gly Leu Pro Ala Thr Pro Leu Leu  
50 55 60  
Phe His Pro His Thr Lys Gly Ser Gln Ile Leu Met Asp Leu Ser His  
65 70 75 80  
Lys Ala Val Lys Arg Gln Ala Ser Phe Cys Asn Ala Ile Thr Phe Ser  
85 90 95



<210> 14  
 <211> 291  
 <212> PRT  
 <213> mouse

<400> 14

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		20						25					30		
Gly	Ser	Phe	Pro	Val	Pro	Ser	His	Arg	Cys	His	His	Lys	Gln	Lys	His
		35				40						45			
Cys	Pro	Pro	Thr	Leu	Ser	Gly	Gly	Gly	Leu	Pro	Ala	Thr	Pro	Leu	Leu
	50					55					60				
Phe	His	Pro	His	Thr	Lys	Gly	Ser	Gln	Ile	Leu	Met	Asp	Leu	Ser	His
65					70					75					80
Lys	Ala	Val	Lys	Arg	Gln	Ala	Ser	Phe	Cys	Asn	Ala	Ile	Thr	Phe	Ser
				85					90					95	
Asn	Arg	Pro	Val	Leu	Ile	Tyr	Glu	Gln	Val	Arg	Leu	Lys	Ile	Thr	Lys
			100					105					110		
Lys	Gln	Cys	Cys	Trp	Ser	Gly	Ala	Leu	Arg	Leu	Gly	Phe	Thr	Ser	Lys
		115				120						125			
Asp	Pro	Ser	Arg	Ile	His	Pro	Asp	Ser	Leu	Pro	Lys	Tyr	Ala	Cys	Pro
		130				135					140				
Asp	Leu	Val	Ser	Gln	Ser	Gly	Phe	Trp	Ala	Lys	Ala	Leu	Pro	Glu	Glu
145					150					155					160
Phe	Ala	Asn	Glu	Gly	Asn	Ile	Ile	Ala	Phe	Trp	Val	Asp	Lys	Lys	Gly
				165					170					175	
Arg	Val	Phe	Tyr	Arg	Ile	Asn	Glu	Ser	Ala	Ala	Met	Leu	Phe	Phe	Ser
			180					185					190		
Gly	Val	Arg	Thr	Val	Asp	Pro	Leu	Trp	Ala	Leu	Val	Asp	Val	Tyr	Gly
		195				200						205			
Leu	Thr	Arg	Gly	Val	Gln	Leu	Leu	Asp	Ser	Glu	Leu	Val	Leu	Pro	Glu
		210				215					220				
Ser	Pro	Val	Thr	Pro	Gly	Leu	Gly	Gln	Trp	Ser	Asp	Glu	Cys	Thr	Ile
225					230					235					240
Cys	Tyr	Glu	His	Ala	Val	Asp	Thr	Val	Ile	Tyr	Thr	Cys	Gly	His	Met
				245					250					255	
Cys	Leu	Cys	Tyr	Ser	Cys	Gly	Leu	Arg	Leu	Lys	Lys	Ala	Leu	His	Ala
			260					265					270		
Cys	Cys	Pro	Ile	Cys	Arg	Arg	Pro	Ile	Lys	Asp	Ile	Ile	Lys	Thr	Tyr
		275					280						285		
Arg	Ser	Ser													
		290													

<210> 15  
 <211> 1725  
 <212> DNA  
 <213> rat

<400> 15

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<212> DNA

<213> rat

<400> 17

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cgatgccatc acaagcagaa gcattgcccg cccgcgtgt caggtggggg gctcccgccc 180
acaccgctgc ttttccaccc ccacactaag ggctcccaga tcctcatgga cctcagccac 240
aaggccgtca agaggcaggc cagcttctgt aatgccatca ccttcagcaa ccgccccgtc 300
ctcatctacg agcaagtcag gctgaagatc accaagaagc agtgcgtctg gagcggggcc 360
ctgcgacttg gcttcaccag caaggaccct tcccgcaccc accccgactc actgcccagg 420
tacgcctgcc ctgacctggg gtcccagagt ggcttctggg ccaaagcggt gcctgaggag 480
tttgccaacg agggcaacat cattgccttc tgggtggaca agaagggccg agtcttctac 540
cggatcaatg agtcggctgc catgctgttc ttcagcgggg ttcgaacggc ggacccgctc 600
tgggccctgg tggacgtcta tggcctcaca cgggggtgtc agctgctagg ctccaccatc 660
atggctgaac ggggtggccc atctctcccc tgctcacctg cctccactcc aacctcgccc 720
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taccgcagct cctag                                     1035
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<210> 18

<211> 344

<212> PRT

<213> rat

<400> 18

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Ser Arg Ala Ser Arg Gly His Pro Gln Asn Leu Lys Asp Ser Ile Gly
 20           25           30
Ser Ser Phe Pro Val Pro Ser His Arg Cys His His Lys Gln Lys His
 35           40           45
Cys Pro Pro Ala Leu Ser Gly Gly Gly Leu Pro Ala Thr Pro Leu Leu
 50           55           60
Phe His Pro His Thr Lys Gly Ser Gln Ile Leu Met Asp Leu Ser His
 65           70           75           80
Lys Ala Val Lys Arg Gln Ala Ser Phe Cys Asn Ala Ile Thr Phe Ser
 85           90           95
Asn Arg Pro Val Leu Ile Tyr Glu Gln Val Arg Leu Lys Ile Thr Lys
100           105           110
Lys Gln Cys Cys Trp Ser Gly Ala Leu Arg Leu Gly Phe Thr Ser Lys
115           120           125
Asp Pro Ser Arg Ile His Pro Asp Ser Leu Pro Lys Tyr Ala Cys Pro
130           135           140
Asp Leu Val Ser Gln Ser Gly Phe Trp Ala Lys Ala Leu Pro Glu Glu
145           150           155           160
Phe Ala Asn Glu Gly Asn Ile Ile Ala Phe Trp Val Asp Lys Lys Gly
165           170           175
Arg Val Phe Tyr Arg Ile Asn Glu Ser Ala Ala Met Leu Phe Phe Ser
180           185           190
Gly Val Arg Thr Ala Asp Pro Leu Trp Ala Leu Val Asp Val Tyr Gly
195           200           205
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Leu Thr Arg Gly Val Gln Leu Leu Gly Ser Thr Ile Met Ala Glu Arg  
 210 215 220  
 Gly Gly Pro Ser Leu Pro Cys Ser Pro Ala Ser Thr Pro Thr Ser Pro  
 225 230 235 240  
 Ser Ala Leu Gly Ser Arg Leu Ser Asp Pro Leu Leu Ser Thr Cys Gly  
 245 250 255  
 Ser Gly Pro Leu Gly Gly Ser Val Gly Gly Thr Ala Pro Asn Ser Pro  
 260 265 270  
 Val Ser Leu Pro Glu Ser Pro Val Thr Pro Gly Leu Gly Gln Trp Ser  
 275 280 285  
 Asp Glu Cys Thr Ile Cys Tyr Glu His Ala Val Asp Thr Val Ile Tyr  
 290 295 300  
 Thr Cys Gly His Met Cys Leu Cys Tyr Ser Cys Gly Leu Arg Leu Lys  
 305 310 315 320  
 Lys Ala Leu His Ala Cys Cys Pro Ile Cys Arg Arg Pro Ile Lys Asp  
 325 330 335  
 Ile Ile Lys Thr Tyr Arg Ser Ser  
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<210> 19  
 <211> 888  
 <212> DNA  
 <213> rat

<400> 19  
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 cgatgccatc acaagcagaa gcattgcccg cccgcgctgt caggtggggg gctcccgcc 180  
 acaccgctgc tcttccaccc ccacactaag ggctcccaga tcctcatgga cctcagccac 240  
 aaggccgtca agaggcaggc cagcttctgt aatgccatca ccttcagcaa ccgccccgtc 300  
 ctcatctacg agcaagtcag gctgaagatc accaagaagc agtgctgctg gagcggggcc 360  
 ctgcgacttg gcttcaccag caaggaccct tcccgcatcc accccgactc actgcccagg 420  
 tacgctgcc ctgacctggg gtcccagagt ggcttctggg ccaaagcggt gcctgaggag 480  
 tttgccaacg agggcaacat cattgccttc tgggtggaca agaagggccg agtcttctac 540  
 cggatcaatg agtcggctgc catgctgttc ttcagcgggg ttcgaacggc ggacccgctc 600  
 tgggccctgg tggacgtcta tggcctcaca cggggtgtcc agctgctagg aacagcccc 660  
 aactcacctg tgagcctgcc cgagtcacca gtgaccccg gtctgggcca gtggagcgat 720  
 gaatgcacca tttgctatga acacgcagt gatacagtca tctacacgtg tggccacatg 780  
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 tgccgtcgcc ccataagga catcatcaag acctaccga gctcctag 888

<210> 20  
 <211> 295  
 <212> PRT  
 <213> rat

<400> 20  
 Met Gly Asn Asn Phe Ser Ser Val Ser Ser Leu Gln Arg Gly Asn Pro  
 1 5 10 15  
 Ser Arg Ala Ser Arg Gly His Pro Gln Asn Leu Lys Asp Ser Ile Gly  
 20 25 30  
 Ser Ser Phe Pro Val Pro Ser His Arg Cys His His Lys Gln Lys His  
 35 40 45  
 Cys Pro Pro Ala Leu Ser Gly Gly Gly Leu Pro Ala Thr Pro Leu Leu

50	55	60
Phe His Pro His Thr Lys Gly Ser Gln Ile Leu Met Asp Leu Ser His		
65	70	75
Lys Ala Val Lys Arg Gln Ala Ser Phe Cys Asn Ala Ile Thr Phe Ser		80
	85	90
Asn Arg Pro Val Leu Ile Tyr Glu Gln Val Arg Leu Lys Ile Thr Lys		95
	100	105
Lys Gln Cys Cys Trp Ser Gly Ala Leu Arg Leu Gly Phe Thr Ser Lys		110
	115	120
Asp Pro Ser Arg Ile His Pro Asp Ser Leu Pro Lys Tyr Ala Cys Pro		125
	130	135
Asp Leu Val Ser Gln Ser Gly Phe Trp Ala Lys Ala Leu Pro Glu Glu		140
145	150	155
Phe Ala Asn Glu Gly Asn Ile Ile Ala Phe Trp Val Asp Lys Lys Gly		160
	165	170
Arg Val Phe Tyr Arg Ile Asn Glu Ser Ala Ala Met Leu Phe Phe Ser		175
	180	185
Gly Val Arg Thr Ala Asp Pro Leu Trp Ala Leu Val Asp Val Tyr Gly		190
	195	200
Leu Thr Arg Gly Val Gln Leu Leu Gly Thr Ala Pro Asn Ser Pro Val		205
	210	215
Ser Leu Pro Glu Ser Pro Val Thr Pro Gly Leu Gly Gln Trp Ser Asp		220
225	230	235
Glu Cys Thr Ile Cys Tyr Glu His Ala Val Asp Thr Val Ile Tyr Thr		240
	245	250
Cys Gly His Met Cys Leu Cys Tyr Ser Cys Gly Leu Arg Leu Lys Lys		255
	260	265
Ala Leu His Ala Cys Cys Pro Ile Cys Arg Arg Pro Ile Lys Asp Ile		270
	275	280
Ile Lys Thr Tyr Arg Ser Ser		285
290	295	

<210> 21

<211> 1675

<212> DNA

<213> Homo sapien

<400> 21

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ttccacgcgc	aggccaaagg	caagaacgtg	cggtctggacg	gccactcgcg	ccggggccaca	180
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gacctggtca	cgcggccggg	ctactggggc	aaggcactgc	ccgagaacct	ggcgctgcgc	420
gacacgggtgc	tggcctactg	ggccgaccgc	cacggcccgcg	tggtctacag	cgatgaacgac	480
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acgcccgcgc	gcctcagcca	ggcccgttc	agcgcctgcc	tgccgcccag	cagccacgac	660
gcggccaact	tcgacaacaa	cgagctcgag	aacaaccagg	tggtggccaa	gctggggccac	720
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tgccggggccc	gtgagcgccc	gcggggccgcg	tcgtcgccgg	cgctactgga	ggccgacctg	840
cgcttccacg	caacacgcgg	gcccgcagctg	agcctgtcgg	ccgaccgcaa	agtggcctgc	900
gcaccgcggc	ccgacggcgg	ccgcacgctg	gtcttctccg	agcggcccgt	gcggggccggc	960

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gagagcctct tcgtggaggt gggccgtccg gggctggcgg cggccggcgc gctggccttc 1020
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atgtgcctgt gccacagctg cggcctgcgg ctcaagcgac agggccgggc ctgctgcccc 1620
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<210> 22

<211> 555

<212> PRT

<213> Homo sapien

<400> 22

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Arg Leu Leu Ala Thr Arg Pro Cys Cys Gly Pro Gly Pro Glu Arg Arg
      20          25          30
Pro Val Leu Gly Glu Ala Pro Arg Phe His Ala Gln Ala Lys Gly Lys
      35          40          45
Asn Val Arg Leu Asp Gly His Ser Arg Arg Ala Thr Arg Arg Asn Ser
      50          55          60
Phe Cys Asn Gly Val Thr Phe Thr Gln Arg Pro Ile Arg Leu Tyr Glu
      65          70          75          80
Gln Val Arg Leu Arg Leu Val Ala Val Arg Pro Gly Trp Ser Gly Ala
      85          90          95
Leu Arg Phe Gly Phe Thr Ala His Asp Pro Ser Leu Met Ser Ala Gln
      100          105          110
Asp Ile Pro Lys Tyr Ala Cys Pro Asp Leu Val Thr Arg Pro Gly Tyr
      115          120          125
Trp Ala Lys Ala Leu Pro Glu Asn Leu Ala Leu Arg Asp Thr Val Leu
      130          135          140
Ala Tyr Trp Ala Asp Arg His Gly Arg Val Phe Tyr Ser Val Asn Asp
      145          150          155          160
Gly Glu Pro Val Leu Phe His Cys Gly Val Ala Val Gly Gly Pro Leu
      165          170          175
Trp Ala Leu Ile Asp Val Tyr Gly Ile Thr Asp Glu Val Gln Leu Leu
      180          185          190
Glu Ser Ala Phe Ala Asp Thr Leu Thr Pro Ala Arg Leu Ser Gln Ala
      195          200          205
Arg Phe Ser Ala Cys Leu Pro Pro Ser Ser His Asp Ala Ala Asn Phe
      210          215          220
Asp Asn Asn Glu Leu Glu Asn Asn Gln Val Val Ala Lys Leu Gly His
      225          230          235          240
Leu Ala Leu Gly Arg Ala Pro Gly Pro Pro Pro Ala Asp Ala Ala Ala
      245          250          255
Ala Ala Ile Pro Cys Gly Pro Arg Glu Arg Pro Arg Pro Ala Ser Ser
      260          265          270
Pro Ala Leu Leu Glu Ala Asp Leu Arg Phe His Ala Thr Arg Gly Pro
      275          280          285

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Asp	Val	Ser	Leu	Ser	Ala	Asp	Arg	Lys	Val	Ala	Cys	Ala	Pro	Arg	Pro
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Asp	Gly	Gly	Arg	Thr	Leu	Val	Phe	Ser	Glu	Arg	Pro	Leu	Arg	Pro	Gly
305					310					315					320
Glu	Ser	Leu	Phe	Val	Glu	Val	Gly	Arg	Pro	Gly	Leu	Ala	Ala	Pro	Gly
				325					330					335	
Ala	Leu	Ala	Phe	Gly	Ile	Thr	Ser	Cys	Asp	Pro	Gly	Val	Leu	Arg	Pro
			340					345					350		
Asn	Glu	Leu	Pro	Ala	Asp	Pro	Asp	Ala	Leu	Leu	Asp	Arg	Lys	Glu	Tyr
		355				360						365			
Trp	Val	Val	Ala	Arg	Ala	Gly	Pro	Val	Pro	Ser	Gly	Gly	Asp	Ala	Leu
	370					375					380				
Ser	Phe	Thr	Leu	Arg	Pro	Gly	Gly	Asp	Val	Leu	Leu	Gly	Ile	Asn	Gly
385					390					395					400
Arg	Pro	Arg	Gly	Arg	Leu	Leu	Cys	Val	Asp	Thr	Thr	Gln	Ala	Leu	Trp
				405					410					415	
Ala	Phe	Phe	Ala	Val	Arg	Gly	Gly	Val	Ala	Gly	Gln	Leu	Arg	Leu	Leu
			420					425					430		
Gly	Thr	Leu	Gln	Ser	Ser	Pro	Ala	Thr	Thr	Thr	Pro	Ser	Gly	Ser	Leu
		435					440					445			
Ser	Gly	Ser	Gln	Asp	Asp	Ser	Asp	Ser	Asp	Met	Thr	Phe	Ser	Val	Asn
	450					455					460				
Gln	Ser	Ser	Ser	Ala	Ser	Glu	Ser	Ser	Leu	Val	Thr	Ala	Pro	Ser	Ser
465					470					475					480
Pro	Leu	Ser	Pro	Pro	Val	Ser	Pro	Val	Phe	Ser	Pro	Pro	Glu	Pro	Ala
				485					490					495	
Gly	Ile	Lys	Asn	Gly	Glu	Cys	Thr	Val	Cys	Phe	Asp	Gly	Glu	Val	Asp
			500					505					510		
Thr	Val	Ile	Tyr	Thr	Cys	Gly	His	Met	Cys	Leu	Cys	His	Ser	Cys	Gly
		515				520						525			
Leu	Arg	Leu	Lys	Arg	Gln	Ala	Arg	Ala	Cys	Cys	Pro	Ile	Cys	Arg	Arg
	530					535					540				
Pro	Ile	Lys	Asp	Val	Ile	Lys	Ile	Tyr	Arg	Pro					
545					550					555					

<210> 23  
 <211> 1129  
 <212> DNA  
 <213> Homo sapien

<400> 23  
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 aacttcgaca acaacgagct cgagaacaac caggtggtgg ccaagctggg ccacctggcg 180  
 ctggggccgcg ccccgggccc accgccagcc gacgccgcgg ccgccgccat tccgtgcggg 240  
 ccccgctgagc gcccgcgccc cgcgctcgctg ccggcgctac tggaggccga cctgcgcttc 300  
 cacgcaacac gcggggccga cgtgagcctg tcggccgacc gcaaagtggc ctgcgcaccg 360  
 cggccccagc gcggccgcac gctggtcttc tccgagcgcc cgctgcggcc cggcgagagc 420  
 ctcttcgctg aggtggggcg tccggggctg gcggcgcccc gcgcgctggc cttcggcatc 480  
 acgtcgtgcg acccgggcgt gctacggccc aacgagctgc ccgccgacct agacgcgctg 540  
 ctcgaccgca aagagtactg ggtggtggcg cgcgccgggc ccgtgccgag cggcgggcgac 600  
 gcgctcagct tcacgctgcg gcccgggcgg gacgtgctcc tgggcatcaa cgggcgtccg 660  
 cgcggccgccc tgctgtgcgt cgacaccacg caggcgctct gggccttctt cgccgtgcgc 720  
 ggcgggcgctg cggggccagct gcgtctcttc ggtaccctgc agtccagccc tgcgaccacg 780

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actccatcag ggtccctcag cggctcccag gacgatagtg attcagatat gaccttcagt 840
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agccccccgg tgtcccccggt gttctcccca ccggagccgg caggcatcaa gaatggcgag 960
tgcacgggtgt gcttcgatgg cgaggtggac acggtcattt acacgtgtgg acacatgtgc 1020
ctgtgccaca gctgcggcct gcggtcgaag cgacaggccc gggcctgctg ccccatctgc 1080
cggcggccca tcaaggacgt cattaagatc tacaggccat agcctagcc 1129

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<210> 24

<211> 373

<212> PRT

<213> Homo sapien

<400> 24

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Met Gly Asn Thr Val His Arg Thr Leu Pro Glu Ser Ala Phe Ala Asp
 1          5          10          15
Thr Leu Thr Pro Ala Arg Leu Ser Gln Ala Arg Phe Ser Ala Cys Leu
 20          25          30
Pro Pro Ser Ser His Asp Ala Ala Asn Phe Asp Asn Asn Glu Leu Glu
 35          40          45
Asn Asn Gln Val Val Ala Lys Leu Gly His Leu Ala Leu Gly Arg Ala
 50          55          60
Pro Gly Pro Pro Pro Ala Asp Ala Ala Ala Ala Ile Pro Cys Gly
 65          70          75          80
Pro Arg Glu Arg Pro Arg Pro Ala Ser Ser Pro Ala Leu Leu Glu Ala
 85          90          95
Asp Leu Arg Phe His Ala Thr Arg Gly Pro Asp Val Ser Leu Ser Ala
 100          105          110
Asp Arg Lys Val Ala Cys Ala Pro Arg Pro Asp Gly Gly Arg Thr Leu
 115          120          125
Val Phe Ser Glu Arg Pro Leu Arg Pro Gly Glu Ser Leu Phe Val Glu
 130          135          140
Val Gly Arg Pro Gly Leu Ala Ala Pro Gly Ala Leu Ala Phe Gly Ile
 145          150          155          160
Thr Ser Cys Asp Pro Gly Val Leu Arg Pro Asn Glu Leu Pro Ala Asp
 165          170          175
Pro Asp Ala Leu Leu Asp Arg Lys Glu Tyr Trp Val Val Ala Arg Ala
 180          185          190
Gly Pro Val Pro Ser Gly Gly Asp Ala Leu Ser Phe Thr Leu Arg Pro
 195          200          205
Gly Gly Asp Val Leu Leu Gly Ile Asn Gly Arg Pro Arg Gly Arg Leu
 210          215          220
Leu Cys Val Asp Thr Thr Gln Ala Leu Trp Ala Phe Phe Ala Val Arg
 225          230          235          240
Gly Gly Val Ala Gly Gln Leu Arg Leu Leu Gly Thr Leu Gln Ser Ser
 245          250          255
Pro Ala Thr Thr Thr Pro Ser Gly Ser Leu Ser Gly Ser Gln Asp Asp
 260          265          270
Ser Asp Ser Asp Met Thr Phe Ser Val Asn Gln Ser Ser Ser Ala Ser
 275          280          285
Glu Ser Ser Leu Val Thr Ala Pro Ser Ser Pro Leu Ser Pro Pro Val
 290          295          300
Ser Pro Val Phe Ser Pro Pro Glu Pro Ala Gly Ile Lys Asn Gly Glu
 305          310          315          320
Cys Thr Val Cys Phe Asp Gly Glu Val Asp Thr Val Ile Tyr Thr Cys
 325          330          335

```

Gly His Met Cys Leu Cys His Ser Cys Gly Leu Arg Leu Lys Arg Gln  
 340 345 350  
 Ala Arg Ala Cys Cys Pro Ile Cys Arg Arg Pro Ile Lys Asp Val Ile  
 355 360 365  
 Lys Ile Tyr Arg Pro  
 370

<210> 25  
 <211> 955  
 <212> DNA  
 <213> Homo sapien

<400> 25  
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 acccggccgt gctgcggccc cggccccgag cgacgcccgg tcctggggcga ggcgccgcgc 120  
 ttccacgcgc aggccaaagg caagaacgtg cggctggacg gccactcgcg ccggggccaca 180  
 cggcgcaaca gcttctgcaa tggcgtcacg ttcacgcagc ggcccatccg gctgtacgag 240  
 caggtgcggc tgcgcctggt ggccgtgcgc cctggctgga gcggcgcgct gcgcttcggc 300  
 ttcaccgcgc acgatccgtc gctcatgagc gcccaggaca tccccaaagta cgcttgcccg 360  
 gacctgggtc cggggccggg ctactggggc aaggcactgc ccgagaacct ggcgctgcgc 420  
 gacacgggtg tggcctactg ggccgaccgc cacggccgcg tgttctacag cgtgaacgac 480  
 ggcgagccgg tgcctttcca ctgcggcggtg gccgtgggag gcccgctctg ggcgctcatt 540  
 gatgtctacg gcataccga cgaggtgcag cttctgggta ccctgcagtc cagccctgcg 600  
 accacgactc catcagggtc cctcagcggc tcccaggacg atagtgattc agatatgacc 660  
 ttcagtgtca accagtcttc ctccgcatct gagtcatccc tggtgacggc cccagctcc 720  
 ccgtgagcc ccccggtgtc ccccggtgtc tccccaccgg agccggcagg catcaagaat 780  
 ggcgagtga cgggtgtgctt cgatggcgag gtggacacgg tcatctacac gtgtggacac 840  
 atgtgcctgt gccacagctg cggcctgcgg ctcaagcgac aggcccgggc ctgctgcccc 900  
 atctgcggc ggcccatcaa ggacgtcatt aagatctaca ggccatagcc tagcc 955

<210> 26  
 <211> 315  
 <212> PRT  
 <213> Homo sapien

<400> 26  
 Met Gly Asn Thr Val His Arg Thr Leu Pro Asp Pro Ser Pro Pro Ala  
 1 5 10 15  
 Arg Leu Leu Ala Thr Arg Pro Cys Cys Gly Pro Gly Pro Glu Arg Arg  
 20 25 30  
 Pro Val Leu Gly Glu Ala Pro Arg Phe His Ala Gln Ala Lys Gly Lys  
 35 40 45  
 Asn Val Arg Leu Asp Gly His Ser Arg Arg Ala Thr Arg Arg Asn Ser  
 50 55 60  
 Phe Cys Asn Gly Val Thr Phe Thr Gln Arg Pro Ile Arg Leu Tyr Glu  
 65 70 75 80  
 Gln Val Arg Leu Arg Leu Val Ala Val Arg Pro Gly Trp Ser Gly Ala  
 85 90 95  
 Leu Arg Phe Gly Phe Thr Ala His Asp Pro Ser Leu Met Ser Ala Gln  
 100 105 110  
 Asp Ile Pro Lys Tyr Ala Cys Pro Asp Leu Val Thr Arg Pro Gly Tyr  
 115 120 125  
 Trp Ala Lys Ala Leu Pro Glu Asn Leu Ala Leu Arg Asp Thr Val Leu  
 130 135 140

Ala	Tyr	Trp	Ala	Asp	Arg	His	Gly	Arg	Val	Phe	Tyr	Ser	Val	Asn	Asp
145					150					155					160
Gly	Glu	Pro	Val	Leu	Phe	His	Cys	Gly	Val	Ala	Val	Gly	Gly	Pro	Leu
				165					170						175
Trp	Ala	Leu	Ile	Asp	Val	Tyr	Gly	Ile	Thr	Asp	Glu	Val	Gln	Leu	Leu
			180					185					190		
Gly	Thr	Leu	Gln	Ser	Ser	Pro	Ala	Thr	Thr	Thr	Pro	Ser	Gly	Ser	Leu
		195					200					205			
Ser	Gly	Ser	Gln	Asp	Asp	Ser	Asp	Ser	Asp	Met	Thr	Phe	Ser	Val	Asn
	210					215					220				
Gln	Ser	Ser	Ser	Ala	Ser	Glu	Ser	Ser	Leu	Val	Thr	Ala	Pro	Ser	Ser
225				230						235					240
Pro	Leu	Ser	Pro	Pro	Val	Ser	Pro	Val	Phe	Ser	Pro	Pro	Glu	Pro	Ala
				245					250					255	
Gly	Ile	Lys	Asn	Gly	Glu	Cys	Thr	Val	Cys	Phe	Asp	Gly	Glu	Val	Asp
			260					265					270		
Thr	Val	Ile	Tyr	Thr	Cys	Gly	His	Met	Cys	Leu	Cys	His	Ser	Cys	Gly
		275					280					285			
Leu	Arg	Leu	Lys	Arg	Gln	Ala	Arg	Ala	Cys	Cys	Pro	Ile	Cys	Arg	Arg
	290				295						300				
Pro	Ile	Lys	Asp	Val	Ile	Lys	Ile	Tyr	Arg	Pro					
305					310					315					

<210> 27  
 <211> 1641  
 <212> DNA  
 <213> Rat

<400> 27  
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 ttccacgcgc aggccaaagg caagaacgtg cgtctagacg gtcactcgcg cagggccacg 180  
 cgacggaaca gcttctgcaa cggagtcacc ttcacgcagc ggcccattcg cctgtacgag 240  
 cagggtgcgg tgcgcctggt ggctgtgctg cctggctgga gcggcgcgct gcgcttcggc 300  
 ttcactgcgc acgacccgtc gctcatgagc gcacaggata tccccaaagta cgctgcccc 360  
 gacctggtca cagcacctgg atactgggccc aaggcgctgc cggagaacct ggcgctgcgg 420  
 gacacgggtg tggcctactg ggctgatcgt cacggtcgcg tcttctatag tgtctatgat 480  
 ggcgaaccag tgctgttcca ctgcggcggtg gccgtgggaa gcccactctg ggcactcatc 540  
 gacgtctatg gcatcacgga cgaggtgcag ctgctggaaa gcacctgcgc agacacgctg 600  
 acccgctgc gcctgggcca ggcgcgcctc agcgctgcc cgcctccggg cagccacgat 660  
 gctgccaaact tcgataataa cgagctggag aataaccagg tggtagccaa gctgggtcac 720  
 ttggctctcg gccgtccgga cgcgcgcgtc ccgtgcgtgg cccgcgaacg cgcgaggccc 780  
 gcttcttcac ccgcgttgct ggacgctgag ctgcgtttcc acgccacgcg cggccccgac 840  
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 gtggtggcgc gcgcggggcc cgtgcccagc ggaggcgacg cactcagctt cacgctgcga 1140  
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 tcagaatcgt ctctggtgac agcccccagc tccccactga gtccccagc gtccccggcc 1440  
 ttctctgcac ccgagccggc cggcagcagg aatggagagt gcacggtgtg cttcgacagc 1500





355	360	365
Pro Ser Gly Gly Asp Ala Leu Ser Phe Thr Leu Arg Pro Gly Gly Asp		
370	375	380
Val Leu Leu Ala Val Asn Gly Arg Pro Arg Gly Arg Leu Leu Cys Val		
385	390	395
Asp Thr Ser Gln Ala Leu Trp Ala Phe Phe Ala Val Arg Gly Gly Val		
405	410	415
Ala Gly Gln Leu Arg Leu Leu Gly Thr Val Gln Ser Gly Pro Glu Ala		
420	425	430
Thr Thr Pro Ser Gly Ser Phe Ser Gly Ser Gln Asp Asp Ser Asp Ser		
435	440	445
Asp Met Thr Phe Gly Val Asn Gln Ser Ser Ser Ala Ser Glu Ser Ser		
450	455	460
Leu Val Thr Ala Pro Ser Ser Pro Leu Ser Pro Pro Val Ser Pro Ala		
465	470	475
Phe Ser Ala Pro Glu Pro Ala Gly Ser Arg Asn Gly Glu Cys Thr Val		
485	490	495
Cys Phe Asp Ser Glu Val Asp Thr Val Ile Tyr Thr Cys Gly His Met		
500	505	510
Cys Leu Cys His Ser Cys Arg Leu Arg Leu Arg Lys Gln Ala Arg Ala		
515	520	525
Cys Cys Pro Ile Cys Arg Arg Pro Ile Lys Asp Val Ile Lys Ile Tyr		
530	535	540
Arg Pro		
545		

<210> 29  
 <211> 789  
 <212> DNA  
 <213> Homo sapien

<400> 29  
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 cgcaccacgt tccacgacgg catcgtgttc agccagcggc cgtgctgcct gggcgagcgt 180  
 gtggcgctgc gactgctgct ggaggagagc ggctggctgc gcggcctccg cgtgggcttc 240  
 acgcgcctgg acccgcgtg cgtgtccgtg cccagcctgc cgcccttcct gtgccccgac 300  
 ctggaggagc agagcccagc gtggggcgcc gtgctgcctg agggctgcgc gctcactggg 360  
 gacttggctc gcttctgggt ggaccgcgc ggctgcctct tcgccaaggt caacgccggc 420  
 tgccggctcc tgetgctga gggcgtgccc gtcggcgccc cgctctgggc cgtgatggac 480  
 gtgtatggga cactaaggc catcgagctg ctggatccca cagccagccg gctcccaaca 540  
 cccatgccat gggacctcag caacaaggct gtgcctgagc ccaaagccac accaggagag 600  
 gagtgtgcca tctgcttcta tcacgtgcc aacaccgcc ttgtgccctg cggccacaca 660  
 tacttctgca gatactgtgc ctggcgggtc ttcagcgata cggccaagt ccctgtgtgc 720  
 cgctggcaga tagaggcggg agccctgcg cagggccctc ctgctctgag ggttgaggaa 780  
 ggctcatga 789

<210> 30  
 <211> 262  
 <212> PRT  
 <213> Homo sapien

<400> 30  
 Met Gly Ala Gln Leu Cys Phe Glu Ala Asn Ala Lys Ala Pro Arg Glu



<210> 32  
 <211> 254  
 <212> PRT  
 <213> mouse

<400> 32

```

Met Gly Ser Leu Leu Ser Pro Glu Ala Asn Ala Glu Val Pro Arg Glu
 1           5           10          15
Ala Leu Ser Phe His Gly Asn Ala Thr Gly Ala Gln Val His Leu Asp
          20          25          30
Asp Gln Arg Ser Thr Ala Arg Arg Arg Ser Thr Phe His Asp Gly Ile
          35          40          45
Val Phe Ser Gln Arg Pro Val Trp Pro Gly Glu Arg Val Ala Leu Arg
          50          55          60
Val Leu Arg His Glu Glu Gly Trp Cys Gly Gly Leu Arg Val Gly Phe
65          70          75          80
Thr Arg Leu Asp Pro Ala Gln Val Ala Ala Ser Cys Leu Pro Pro Phe
          85          90          95
Val Cys Pro Asp Leu Glu Glu Gln Ser Pro Thr Trp Ala Ala Leu Leu
          100         105         110
Pro Glu Gly Phe Val Arg Ala Gly Asn Val Val Cys Phe Trp Val Asn
          115         120         125
Arg Arg Gly Trp Leu Phe Ala Lys Val Asn Ala Gly Arg Pro Leu Leu
          130         135         140
Leu Arg Lys Asp Val Leu Val Gln Gly Ala Pro Leu Trp Ala Val Met
145         150         155         160
Asp Val Tyr Gly Thr Thr Lys Ala Ile Glu Leu Leu Asp Pro Lys Ala
          165         170         175
Asn Ala Trp Ile Arg Ser Gly Glu Pro Val Pro Glu Ser Glu Val Ile
          180         185         190
Ser Gly Glu Glu Cys Val Ile Cys Phe His Asn Thr Ala Asn Thr Arg
          195         200         205
Leu Met Pro Cys Gly His Ser His Phe Cys Gly Ser Cys Ala Trp His
          210         215         220
Ile Phe Lys Asp Thr Ala Arg Cys Pro Ile Cys Arg Trp Gln Ile Glu
225         230         235         240
Glu Val Ala Val Val Ser Ser Leu Lys Ala Glu Glu Gly Ser
          245         250

```

<210> 33  
 <211> 250  
 <212> DNA  
 <213> Homo sapien

<400> 33

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cgcttccatc ggggtgcacgg tgccaacatc cgcgtggacc cctctgggac gcgggccaca 60
cgcgtggaga gcttcgcca cggcgtgtgc ttcagccgag agccgctggc cccgggccag 120
gtcttcctgg tcgagatcga ggagaaagag ctgggctggg gcggacatct gcgtctcggg 180
ctgaccgcgc tggaccccg cagtctggcc cccgttcccg agttttctct gcccgatctg 240
gtcaacctgg                250

```

<210> 34  
 <211> 83  
 <212> PRT

<213> Homo sapien

<400> 34

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Arg Phe His Arg Val His Gly Ala Asn Ile Arg Val Asp Pro Ser Gly
 1           5           10          15
Thr Arg Ala Thr Arg Val Glu Ser Phe Ala His Gly Val Cys Phe Ser
      20           25           30
Arg Glu Pro Leu Ala Pro Gly Gln Val Phe Leu Val Glu Ile Glu Glu
      35           40           45
Lys Glu Leu Gly Trp Cys Gly His Leu Arg Leu Gly Leu Thr Ala Leu
      50           55           60
Asp Pro Ala Ser Leu Ala Pro Val Pro Glu Phe Ser Leu Pro Asp Leu
65           70           75           80
Val Asn Leu
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<210> 35

<211> 1743

<212> DNA

<213> rat

<400> 35

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gcgttgcaatt tactgaagag tggctgcagc cctgcggttc agattaaaat tcgagaatta 180
tacagacgcc gatacccacg gacacttgaa ggactttctg atctatccac aatcaaactct 240
tcagttttca gtttgatgg tagctcatca ccagtagagc ctgacttggc cgtggctggg 300
atccactcgt tgccctctac ttccattgca cctcattcac cgtcatctcc tgtcgttct 360
gtgctgcttc aagacactaa gcccacgttt gagatgcagc aaccatctcc tcccattcct 420
cctgtccatc ctgacgtgca gttaaaaacg ctgcccttct atgacgtcct tgatgttctc 480
atcaagccca caagtttagt tcaaagcagt attcagcggg ttcaagagaa gttttttatt 540
tttgctttga cccccagca agttagagag atatgcattt caagggattt tttgccagg 600
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cctcaagaag ataactatcc caatagtttg tgtataaaag taaatgggaa actctttcct 720
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tgggcacatg aaattggaaa gaattactcc atgtctgtgt atcttgtacg acagettaca 900
tcagccatgt tattacagag attaaaaatg aaaggatta gaaatcctga tcattccaaa 960
gcactcatta aagaaaaact tactgcagat cctgatagtg aaattgctac aactagtctt 1020
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tgtacaaaag tagaaagttc aagtgtcttt agtaaacctt gttcagtgac tgtagccagt 1380
gatgcaagca agaagaagat tgatgttatt gatctaacia tagagagctc ttctgatgaa 1440
gaggaagacc ctcccgccaa aaggaaatgc atctttatgt cagaaacaca aagcagtcca 1500
accaaagggg ttctcatgta tcagccatct tctgtaaggg tgcccagtgt gacttcagtt 1560
gatcctgctg ctattccacc ttcatataca gactactcag taccattcca ccacacgcca 1620
gtgtcgagca tgtcatcaga tttgccaggg ttggattttc tttcccttat tccagttgat 1680
ccccagtctc acctcaccct taacagcaag cagtacgtct gtcaccacca ccagccccc 1740
tga 1743
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<210> 36

<211> 580

<212> PRT

<213> rat

<400> 36

Met	Ala	Asp	Phe	Glu	Glu	Leu	Arg	Asn	Met	Val	Ser	Ser	Phe	Arg	Val
1				5				10					15		
Ser	Glu	Leu	Gln	Val	Leu	Leu	Gly	Phe	Ala	Gly	Arg	Asn	Lys	Ser	Gly
			20					25					30		
Arg	Lys	His	Asp	Leu	Leu	Met	Arg	Ala	Leu	His	Leu	Leu	Lys	Ser	Gly
		35					40					45			
Cys	Ser	Pro	Ala	Val	Gln	Ile	Lys	Ile	Arg	Glu	Leu	Tyr	Arg	Arg	Arg
	50					55				60					
Tyr	Pro	Arg	Thr	Leu	Glu	Gly	Leu	Ser	Asp	Leu	Ser	Thr	Ile	Lys	Ser
65					70					75				80	
Ser	Val	Phe	Ser	Leu	Asp	Gly	Ser	Ser	Ser	Pro	Val	Glu	Pro	Asp	Leu
				85				90						95	
Ala	Val	Ala	Gly	Ile	His	Ser	Leu	Pro	Ser	Thr	Ser	Ile	Ala	Pro	His
			100					105					110		
Ser	Pro	Ser	Ser	Pro	Val	Ala	Ser	Val	Leu	Leu	Gln	Asp	Thr	Lys	Pro
		115					120					125			
Thr	Phe	Glu	Met	Gln	Gln	Pro	Ser	Pro	Pro	Ile	Pro	Pro	Val	His	Pro
	130					135					140				
Asp	Val	Gln	Leu	Lys	Thr	Leu	Pro	Phe	Tyr	Asp	Val	Leu	Asp	Val	Leu
145					150					155				160	
Ile	Lys	Pro	Thr	Ser	Leu	Val	Gln	Ser	Ser	Ile	Gln	Arg	Phe	Gln	Glu
				165					170					175	
Lys	Phe	Phe	Ile	Phe	Ala	Leu	Thr	Pro	Gln	Gln	Val	Arg	Glu	Ile	Cys
			180					185					190		
Ile	Ser	Arg	Asp	Phe	Leu	Pro	Gly	Gly	Arg	Arg	Asp	Tyr	Thr	Val	Gln
		195					200					205			
Val	Gln	Leu	Arg	Leu	Cys	Leu	Ala	Glu	Thr	Ser	Cys	Pro	Gln	Glu	Asp
	210					215					220				
Asn	Tyr	Pro	Asn	Ser	Leu	Cys	Ile	Lys	Val	Asn	Gly	Lys	Leu	Phe	Pro
225					230					235				240	
Leu	Pro	Gly	Tyr	Ala	Pro	Pro	Pro	Lys	Asn	Gly	Ile	Glu	Gln	Lys	Arg
				245					250					255	
Pro	Gly	Arg	Pro	Leu	Asn	Ile	Thr	Ser	Leu	Val	Arg	Leu	Ser	Ser	Ala
			260					265					270		
Val	Pro	Asn	Gln	Ile	Ser	Ile	Ser	Trp	Ala	Ser	Glu	Ile	Gly	Lys	Asn
		275					280					285			
Tyr	Ser	Met	Ser	Val	Tyr	Leu	Val	Arg	Gln	Leu	Thr	Ser	Ala	Met	Leu
	290					295					300				
Leu	Gln	Arg	Leu	Lys	Met	Lys	Gly	Ile	Arg	Asn	Pro	Asp	His	Ser	Lys
305					310					315				320	
Ala	Leu	Ile	Lys	Glu	Lys	Leu	Thr	Ala	Asp	Pro	Asp	Ser	Glu	Ile	Ala
				325					330					335	
Thr	Thr	Ser	Leu	Arg	Val	Ser	Leu	Met	Cys	Pro	Leu	Gly	Lys	Met	Arg
			340					345					350		
Leu	Thr	Ile	Pro	Cys	Arg	Ala	Val	Thr	Cys	Thr	His	Leu	Gln	Cys	Phe
		355					360					365			
Asp	Ala	Ala	Leu	Tyr	Leu	Gln	Met	Asn	Glu	Lys	Lys	Pro	Thr	Trp	Ile
	370					375					380				
Cys	Pro	Val	Cys	Asp	Lys	Lys	Ala	Ala	Tyr	Glu	Ser	Leu	Ile	Leu	Asp
385					390					395					400

Gly Leu Phe Met Glu Ile Leu Asn Asp Cys Ser Asp Val Asp Glu Ile  
405 410 415  
Lys Phe Gln Glu Asp Gly Ser Trp Cys Pro Met Arg Pro Lys Lys Glu  
420 425 430  
Ala Met Lys Val Thr Ser Gln Pro Cys Thr Lys Val Glu Ser Ser Ser  
435 440 445  
Val Phe Ser Lys Pro Cys Ser Val Thr Val Ala Ser Asp Ala Ser Lys  
450 455 460  
Lys Lys Ile Asp Val Ile Asp Leu Thr Ile Glu Ser Ser Ser Asp Glu  
465 470 475 480  
Glu Glu Asp Pro Pro Ala Lys Arg Lys Cys Ile Phe Met Ser Glu Thr  
485 490 495  
Gln Ser Ser Pro Thr Lys Gly Val Leu Met Tyr Gln Pro Ser Ser Val  
500 505 510  
Arg Val Pro Ser Val Thr Ser Val Asp Pro Ala Ala Ile Pro Pro Ser  
515 520 525  
Leu Thr Asp Tyr Ser Val Pro Phe His His Thr Pro Val Ser Ser Met  
530 535 540  
Ser Ser Asp Leu Pro Gly Leu Asp Phe Leu Ser Leu Ile Pro Val Asp  
545 550 555 560  
Pro Gln Ser His Leu Thr Leu Asn Ser Lys Gln Tyr Val Cys His His  
565 570 575  
His Gln Pro Pro  
580

<210> 37  
<211> 1251  
<212> DNA  
<213> Homo sapien

<400> 37  
atgagcacca agcagatcac ttgcaggtat tttatgcatg gtgtgtgtcg ggaaggaagt 60  
cagtgcctat tctcacatga cttggcaaac agcaaaccgt ccaccatctg caagtactac 120  
cagaagggct actgtgccta tggaaactcg tgcagatatg accacacgag gccctctgct 180  
gcagctggag gtgtgtgtgg caccatggcc cacagtgtgc cctccccagc tttccacagt 240  
cctcaccctc cttccgaggt cactgcatcc attgtgaaaa ctaactcaca tgaaccgga 300  
aagcgtgaaa agagaacatt ggttcttaga gaccgaaatc tctctggcat ggctgaaagg 360  
aagaccgagc cgagcatggt gagtaatcca ggcagctgca gcgaccccca gccagcccc 420  
gagatgaagc cgcattccta cctggatgcc atcaggagtg gccttgatga cgtggaggcc 480  
agcagctcct acagcaacga gcagcagctg tgcccctacg cagctgctgg ggagtgccgg 540  
tttggggatg cctgtgtcta cctgcacggg gaggtgtgtg aaatctgtag gctgcaagtc 600  
ttgcacccat tcgacccaga gcagaggaag gctcatgaaa agatctgcat gttgacgttc 660  
gaacacgaga tggaaaaggc ctttgccttc caggcaagcc aggacaaagt gtgcagtatc 720  
tgcatggaag tgatcctgga gaaggcctct gcttctgaga ggagatttgg gattctctcc 780  
aattgcaatc acacgtactg tttgtcctgc atccggcagt ggcggtgtgc cgaacagttt 840  
gaaaacccaa tcattaagtc ttgtccagaa tgccgtgtga tatcagagtt tgaattcca 900  
agtgtgtatt ggggtggaaga tcagaataaa aagaacgagt tgattgaagc tttcaaacag 960  
gggatgggga aaaaagcctg taaatacttt gagcaaggca aggggacctg cccatttggg 1020  
agcaaatgtc tttatcgcca tgcttacccc gatgggcggc tagcagagcc tgagaaacct 1080  
cggaacagc tcagttctca aggcactgtg aggttcttta attcagtgcg gctctgggat 1140  
ttcatcgaga accgagaaag ccggcatgtc cccaacaatg aagatgtcga catgacagag 1200  
ctcggggacc tcttcatgca cctttctgga gtggaatcat cagaacccta a 1251

<210> 38

<211> 416  
 <212> PRT  
 <213> Homo sapien

<400> 38

Met	Ser	Thr	Lys	Gln	Ile	Thr	Cys	Arg	Tyr	Phe	Met	His	Gly	Val	Cys		
1				5					10					15			
Arg	Glu	Gly	Ser	Gln	Cys	Leu	Phe	Ser	His	Asp	Leu	Ala	Asn	Ser	Lys		
			20					25					30				
Pro	Ser	Thr	Ile	Cys	Lys	Tyr	Tyr	Gln	Lys	Gly	Tyr	Cys	Ala	Tyr	Gly		
		35				40						45					
Thr	Arg	Cys	Arg	Tyr	Asp	His	Thr	Arg	Pro	Ser	Ala	Ala	Ala	Gly	Gly		
	50					55					60						
Ala	Val	Gly	Thr	Met	Ala	His	Ser	Val	Pro	Ser	Pro	Ala	Phe	His	Ser		
65					70					75					80		
Pro	His	Pro	Pro	Ser	Glu	Val	Thr	Ala	Ser	Ile	Val	Lys	Thr	Asn	Ser		
				85					90					95			
His	Glu	Pro	Gly	Lys	Arg	Glu	Lys	Arg	Thr	Leu	Val	Leu	Arg	Asp	Arg		
			100					105					110				
Asn	Leu	Ser	Gly	Met	Ala	Glu	Arg	Lys	Thr	Gln	Pro	Ser	Met	Val	Ser		
		115						120					125				
Asn	Pro	Gly	Ser	Cys	Ser	Asp	Pro	Gln	Pro	Ser	Pro	Glu	Met	Lys	Pro		
	130					135					140						
His	Ser	Tyr	Leu	Asp	Ala	Ile	Arg	Ser	Gly	Leu	Asp	Asp	Val	Glu	Ala		
145					150					155					160		
Ser	Ser	Ser	Tyr	Ser	Asn	Glu	Gln	Gln	Leu	Cys	Pro	Tyr	Ala	Ala	Ala		
				165					170					175			
Gly	Glu	Cys	Arg	Phe	Gly	Asp	Ala	Cys	Val	Tyr	Leu	His	Gly	Glu	Val		
			180					185					190				
Cys	Glu	Ile	Cys	Arg	Leu	Gln	Val	Leu	His	Pro	Phe	Asp	Pro	Glu	Gln		
		195				200						205					
Arg	Lys	Ala	His	Glu	Lys	Ile	Cys	Met	Leu	Thr	Phe	Glu	His	Glu	Met		
	210					215					220						
Glu	Lys	Ala	Phe	Ala	Phe	Gln	Ala	Ser	Gln	Asp	Lys	Val	Cys	Ser	Ile		
225					230					235					240		
Cys	Met	Glu	Val	Ile	Leu	Glu	Lys	Ala	Ser	Ala	Ser	Glu	Arg	Arg	Phe		
				245					250					255			
Gly	Ile	Leu	Ser	Asn	Cys	Asn	His	Thr	Tyr	Cys	Leu	Ser	Cys	Ile	Arg		
		260						265					270				
Gln	Trp	Arg	Cys	Ala	Glu	Gln	Phe	Glu	Asn	Pro	Ile	Ile	Lys	Ser	Cys		
		275					280						285				
Pro	Glu	Cys	Arg	Val	Ile	Ser	Glu	Phe	Val	Ile	Pro	Ser	Val	Tyr	Trp		
	290					295					300						
Val	Glu	Asp	Gln	Asn	Lys	Lys	Asn	Glu	Leu	Ile	Glu	Ala	Phe	Lys	Gln		
305					310					315					320		
Gly	Met	Gly	Lys	Lys	Ala	Cys	Lys	Tyr	Phe	Glu	Gln	Gly	Lys	Gly	Thr		
				325					330					335			
Cys	Pro	Phe	Gly	Ser	Lys	Cys	Leu	Tyr	Arg	His	Ala	Tyr	Pro	Asp	Gly		
		340						345					350				
Arg	Leu	Ala	Glu	Pro	Glu	Lys	Pro	Arg	Lys	Gln	Leu	Ser	Ser	Gln	Gly		
		355					360						365				
Thr	Val	Arg	Phe	Phe	Asn	Ser	Val	Arg	Leu	Trp	Asp	Phe	Ile	Glu	Asn		
	370					375					380						
Arg	Glu	Ser	Arg	His	Val	Pro	Asn	Asn	Glu	Asp	Val	Asp	Met	Thr	Glu		
385					390					395					400		

Leu Gly Asp Leu Phe Met His Leu Ser Gly Val Glu Ser Ser Glu Pro  
 405 410 415

<210> 39  
 <211> 738  
 <212> DNA  
 <213> Homo sapien

<400> 39  
 atgaaacgga ggaagcaaga tgaagggcag aggggaaggct cctgcatggc tgaggatgat 60  
 gctgtggaca tgcagcatga gaacaacaac cgctttgagg agtatgagtg gtgtggacag 120  
 aagcggatac gggccaccac tctcctggaa ggtggcttcc gaggtctctgg cttcatcatg 180  
 tgcagcggca aagagaaccc ggacagtgat gctgacttgg atgtggatgg ggatgacact 240  
 ctggagtatg ggaagccaca atacacagag gctgatgtca tcccctgcac aggcgaggag 300  
 cctggtgaag ccaaggagag agaggcactt cggggcgagcgcag tcctaaatgg cggccctccc 360  
 agcacgcgca tcacacctga gttctctaaa tggggccagtg atgagatgcc atccaccagc 420  
 aatggtgaaa gcagcaagca ggaggccatg cagaagacct gcaagaacag cgacatcgag 480  
 aaaatcaccg aagattcagc tgtgaccacg tttgaggctc tgaaggctcg ggtcagagaa 540  
 cttgaacggc agctatctcg tggggaccgt tacaatgcc tcatctgcat ggactcgtac 600  
 tcgatgcccc taacgtccat ccagtgttgg cacgtgcact gcgaggagtg ctggctgctg 660  
 accctgggtg ccaagaagct ctgccctcag tgcaacacga tcacagcgcc cggagacctg 720  
 cggaggatct acttgtga 738

<210> 40  
 <211> 245  
 <212> PRT  
 <213> Homo sapien

<400> 40  
 Met Lys Arg Arg Lys Gln Asp Glu Gly Gln Arg Glu Gly Ser Cys Met  
 1 5 10 15  
 Ala Glu Asp Asp Ala Val Asp Ile Glu His Glu Asn Asn Asn Arg Phe  
 20 25 30  
 Glu Glu Tyr Glu Trp Cys Gly Gln Lys Arg Ile Arg Ala Thr Thr Leu  
 35 40 45  
 Leu Glu Gly Gly Phe Arg Gly Ser Gly Phe Ile Met Cys Ser Gly Lys  
 50 55 60  
 Glu Asn Pro Asp Ser Asp Ala Asp Leu Asp Val Asp Gly Asp Asp Thr  
 65 70 75 80  
 Leu Glu Tyr Gly Lys Pro Gln Tyr Thr Glu Ala Asp Val Ile Pro Cys  
 85 90 95  
 Thr Gly Glu Glu Pro Gly Glu Ala Lys Glu Arg Glu Ala Leu Arg Gly  
 100 105 110  
 Ala Val Leu Asn Gly Gly Pro Pro Ser Thr Arg Ile Thr Pro Glu Phe  
 115 120 125  
 Ser Lys Trp Ala Ser Asp Glu Met Pro Ser Thr Ser Asn Gly Glu Ser  
 130 135 140  
 Ser Lys Gln Glu Ala Met Gln Lys Thr Cys Lys Asn Ser Asp Ile Glu  
 145 150 155 160  
 Lys Ile Thr Glu Asp Ser Ala Val Thr Thr Phe Glu Ala Leu Lys Ala  
 165 170 175  
 Arg Val Arg Glu Leu Glu Arg Gln Leu Ser Arg Gly Asp Arg Tyr Lys  
 180 185 190  
 Cys Leu Ile Cys Met Asp Ser Tyr Ser Met Pro Leu Thr Ser Ile Gln



195	200	205
Cys Trp His Val His Cys Glu Glu Cys Trp Leu Arg Thr Leu Gly Ala		
210	215	220
Lys Lys Leu Cys Pro Gln Cys Asn Thr Ile Thr Ala Pro Gly Asp Leu		
225	230	235
Arg Arg Ile Tyr Leu		240
245		

<210> 41  
 <211> 1425  
 <212> DNA  
 <213> Homo sapien

<400> 41  
 atgtcgtcag aagatcgaga agctcaggag gatgaattgc tggccctggc aagtattttac 60  
 gatggagatg aatttagaaa agcagagtct gtccaagggt gagaaaccag gatctatttg 120  
 gatttgccac agaatttcaa gatatttgtg agcggcaatt caaatgagtg tctccagaat 180  
 agtggtcttg aatacaccat ttgctttctg cctccacttg tgctgaactt tgaactgcc 240  
 ccagattatc catcctcttc cccaccttca ttcacactta gtggcaaatg gctgtcacca 300  
 actcagctat ctgctctatg caagcactta gacaacctat gggaagaaca ccgtggcagc 360  
 gtggtcctgt ttgcttggat gcaatttctt aaggaagaga ccctagcata cttgaatatt 420  
 gtctctcctt ttgagctcaa gattgggttct cagaaaaaag tgcagagaag gacagctcaa 480  
 gcttctccca acacagagct agattttgga ggagctgctg gatctgatgt agaccaagag 540  
 gaaattgtgg atgagagagc agtgcaggat gtggaatcac tgtcaaatct gatccaggaa 600  
 atcttggact ttgatcaagc tcagcagata aaatgcttta atagtaaatt gttcctgtgc 660  
 agtatctgtt tctgtgagaa gctgggtagt gaatgcatgt acttcttggg gtgcaggcat 720  
 gtgtactgca aagcctgtct gaaggactac tttgaaatcc agatcagaga tggccagggt 780  
 caatgcctca actgccaga accaaagtgc cttcgggtgg ccactcctgg tcagggtcaa 840  
 gagttagtgg aagcagagtt atttgcccgt tatgaccgcc ttctcctcca gtcctccttg 900  
 gacctgatgg cagatgtggt gtactgcccc cggcctgtgt gccagctgcc tgtgatgcag 960  
 gaacctggct gcaccatggg tatctgctcc agctgcaatt ttgccttctg tactttgtgc 1020  
 aggttgacct accatgggggt ctccccatgt aaggtgactg cagagaaatt aatggactta 1080  
 cgaaatgaat acctgcaagc ggatgaggct aataaaagac ttttggatca aaggtatggt 1140  
 aagagagtga ttcagaaggc actggaagag atggaaagta aggagtggct agagaagaac 1200  
 tcaaagagct gcccatgttg tggaaactccc atagagaaat tagacggatg taacaagatg 1260  
 acatgtactg gctgtatgca atatttctgt tggatttgca tgggttctct ctctagagca 1320  
 aacccttaca aacatttcaa tgacctggt tcaccatgtt ttaaccggct gttttatgct 1380  
 gtggatgttg acgacgatat ttgggaagat gaggtagaag actag 1425

<210> 42  
 <211> 474  
 <212> PRT  
 <213> Homo sapien

<400> 42  
 Met Ser Ser Glu Asp Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu  
 1 5 10 15  
 Ala Ser Ile Tyr Asp Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln  
 20 25 30  
 Gly Gly Glu Thr Arg Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile  
 35 40 45  
 Phe Val Ser Gly Asn Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu  
 50 55 60  
 Tyr Thr Ile Cys Phe Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro

65	Pro	Asp	Tyr	Pro	Ser	Ser	Ser	Pro	Pro	Ser	Phe	Thr	Leu	Ser	Gly	Lys	80
					85					90					95		
Trp	Leu	Ser	Pro	Thr	Gln	Leu	Ser	Ala	Leu	Cys	Lys	His	Leu	Asp	Asn		
			100					105					110				
Leu	Trp	Glu	Glu	His	Arg	Gly	Ser	Val	Val	Leu	Phe	Ala	Trp	Met	Gln		
		115					120					125					
Phe	Leu	Lys	Glu	Glu	Thr	Leu	Ala	Tyr	Leu	Asn	Ile	Val	Ser	Pro	Phe		
		130				135					140						
Glu	Leu	Lys	Ile	Gly	Ser	Gln	Lys	Lys	Val	Gln	Arg	Arg	Thr	Ala	Gln		
145					150					155					160		
Ala	Ser	Pro	Asn	Thr	Glu	Leu	Asp	Phe	Gly	Gly	Ala	Ala	Gly	Ser	Asp		
			165						170					175			
Val	Asp	Gln	Glu	Glu	Ile	Val	Asp	Glu	Arg	Ala	Val	Gln	Asp	Val	Glu		
		180					185						190				
Ser	Leu	Ser	Asn	Leu	Ile	Gln	Glu	Ile	Leu	Asp	Phe	Asp	Gln	Ala	Gln		
		195					200					205					
Gln	Ile	Lys	Cys	Phe	Asn	Ser	Lys	Leu	Phe	Leu	Cys	Ser	Ile	Cys	Phe		
	210					215					220						
Cys	Glu	Lys	Leu	Gly	Ser	Glu	Cys	Met	Tyr	Phe	Leu	Glu	Cys	Arg	His		
225					230					235					240		
Val	Tyr	Cys	Lys	Ala	Cys	Leu	Lys	Asp	Tyr	Phe	Glu	Ile	Gln	Ile	Arg		
			245						250					255			
Asp	Gly	Gln	Val	Gln	Cys	Leu	Asn	Cys	Pro	Glu	Pro	Lys	Cys	Pro	Ser		
		260						265					270				
Val	Ala	Thr	Pro	Gly	Gln	Val	Lys	Glu	Leu	Val	Glu	Ala	Glu	Leu	Phe		
		275					280					285					
Ala	Arg	Tyr	Asp	Arg	Leu	Leu	Leu	Gln	Ser	Ser	Leu	Asp	Leu	Met	Ala		
		290				295					300						
Asp	Val	Val	Tyr	Cys	Pro	Arg	Pro	Cys	Cys	Gln	Leu	Pro	Val	Met	Gln		
305					310					315					320		
Glu	Pro	Gly	Cys	Thr	Met	Gly	Ile	Cys	Ser	Ser	Cys	Asn	Phe	Ala	Phe		
			325						330					335			
Cys	Thr	Leu	Cys	Arg	Leu	Thr	Tyr	His	Gly	Val	Ser	Pro	Cys	Lys	Val		
		340						345					350				
Thr	Ala	Glu	Lys	Leu	Met	Asp	Leu	Arg	Asn	Glu	Tyr	Leu	Gln	Ala	Asp		
		355					360						365				
Glu	Ala	Asn	Lys	Arg	Leu	Leu	Asp	Gln	Arg	Tyr	Gly	Lys	Arg	Val	Ile		
		370				375					380						
Gln	Lys	Ala	Leu	Glu	Glu	Met	Glu	Ser	Lys	Glu	Trp	Leu	Glu	Lys	Asn		
385					390					395					400		
Ser	Lys	Ser	Cys	Pro	Cys	Cys	Gly	Thr	Pro	Ile	Glu	Lys	Leu	Asp	Gly		
			405						410					415			
Cys	Asn	Lys	Met	Thr	Cys	Thr	Gly	Cys	Met	Gln	Tyr	Phe	Cys	Trp	Ile		
		420						425					430				
Cys	Met	Gly	Ser	Leu	Ser	Arg	Ala	Asn	Pro	Tyr	Lys	His	Phe	Asn	Asp		
		435					440					445					
Pro	Gly	Ser	Pro	Cys	Phe	Asn	Arg	Leu	Phe	Tyr	Ala	Val	Asp	Val	Asp		
		450				455					460						
Asp	Asp	Ile	Trp	Glu	Asp	Glu	Val	Glu	Asp								
465					470												

<210> 43

<211> 6

<212> PRT  
<213> Artificial Sequence

<220>  
<223> nuclear localization signal

<400> 43  
His Lys Ala Val Lys Arg  
1 5

<210> 44  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> nuclear localization signal

<400> 44  
Arg Leu Lys Ile Thr Lys Lys  
1 5

<210> 45  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> putative protein kinase phosphorylation site

<400> 45  
Arg Pro Arg Ser Phe Thr  
1 5

<210> 46  
<211> 7  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> protein kinase phosphorylation site consensus  
sequence

<221> VARIANT  
<222> 2, 4, 5  
<223> Xaa = any amino acid

<400> 46  
Arg Xaa Arg Xaa Xaa Ser Thr  
1 5

<210> 47  
<211> 24  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> consensus sequence

<221> VARIANT  
<222> 3, 5, 8, 10, 12, 15, 16, 17, 19, 20, 21, 22  
<223> Xaa = any amino acid

<400> 47  
Ser Thr Xaa Pro Xaa Ser Pro Xaa Ser Xaa Pro Xaa Ser Pro Xaa Xaa  
1 5 10 15  
Xaa Gly Xaa Xaa Xaa Xaa Ser Asp  
20

<210> 48  
<211> 9  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> neuralized homology repeat domain

<400> 48  
Leu Pro Lys Tyr Ala Cys Pro Asp Leu  
1 5